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Figure 1

Frame 2

ATG	CAT	GGA	GTG	GAC	CTG	TAG	GCG	ACT	TGC	ATC	GTC	TTC	AAC	M	K	I	A
		10			19			28			37			46			55
T	V	S	V	L	L	P	L	A	L	C	L	I	Q	D	A	A	S
ACA	GTG	TCA	GTG	CTT	CTG	CCC	TTG	GCT	CTT	TGC	CTC	ATA	CAA	GAT	GCT	GCC	AGT
		64			73			82			91			100			109
Repeat 1																	
E	D	Q	E	M	C	H	E	F	Q	A	F	M	K	N	G	K	L
GAA	GAT	CAG	GAA	ATG	TGC	CAT	GAA	TTT	CAG	GCA	TTT	ATG	AAA	AAT	GGA	AAA	CTG
		124			133			142			151			160			169
P	Q	D	K	K	F	F	Q	S	L	D	G	I	M	F	I	N	K
CCC	CAG	GAT	AAG	AAA	TTT	TTT	CAA	AGT	CTT	GAT	GGA	ATA	ATG	TTC	ATC	AAT	AAA
		184			193			202			211			220			229
HF 6479																	
T	C	K	M	I	L	E	K	E	A	K	S	Q	K	R	A	R	H
ACG	TGC	AAA	ATG	ATA	CTG	GAA	AAA	GAA	GCA	AAA	TCA	CAG	AAG	AGG	GCC	AGG	CAT
		244			253			262			271			280			289
typical Kazal domain 1																	
R	A	P	K	A	T	A	P	T	E	L	N	C	D	D	F	K	K
AGA	GCT	CCC	AAG	GCT	ACT	GCC	CCA	ACA	GAG	CTG	AAT	TGT	GAT	GAT	TTT	AAA	AAA
		304			313			322			331			340			349
R	D	G	D	F	I	C	P	D	Y	Y	E	A	V	C	G	T	D
AGA	GAT	GGG	GAT	TTT	ATC	TGT	CCT	GAT	TAT	TAT	GAA	GCT	GTT	TGT	GGC	ACA	GAT
		364			373			382			391			400			409
T	Y	D	N	R	C	A	L	C	A	E	N	A	K	T	G	S	Q
ACA	TAT	GAC	AAC	AGA	TGT	GCA	CTG	TGT	GCT	GAG	AAT	GCG	AAA	ACC	GGG	TCC	CAA
		424			433			442			451			460			469
Repeat 2																	
V	K	S	E	G	E	C	K	S	S	N	P	E	Q	D	V	C	S
GTA	AAA	AGT	GAA	GGG	GAA	TGT	AAG	AGC	AGT	AAT	CCA	GAG	CAG	GAT	GTA	TGC	AGT
		484			493			502			511			520			529
R	P	F	V	R	D	G	R	L	G	C	T	R	E	N	D	P	V
CGG	CCC	TTT	GTT	AGA	GAT	GGA	AGA	CTT	GGA	TGC	ACA	AGG	GAA	AAT	GAT	CCT	GTT
		544			553			562			571			580			589
P	D	G	K	T	H	G	N	K	C	A	M	C	A	E	L	F	L
CCT	GAT	GGG	AAG	ACG	CAT	GGC	AAT	AAG	TGT	GCA	ATG	TGT	GCT	GAG	CTG	TTT	TTA
		604			613			622			631			640			649
A	E	N	A	K	R	E	G	E	T	R	I	R	R	N	A	E	K
GCT	GAA	AAT	GCC	AAG	CGA	GAG	GGT	GAA	ACT	AGA	ATT	CGA	CGA	AAT	GCT	GAA	AAG
		664			673			682			691			700			709
Repeat 3																	
C	K	E	Y	E	K	Q	V	R	N	G	R	L	F	C	T	R	E
TGC	AAG	GAA	TAT	GAA	AAA	CAA	GTG	AGA	AAT	GGA	AGG	CTT	TTT	TGT	ACA	CGG	GAG
		724			733			742			751			760			769
P	V	R	G	P	D	G	R	M	H	G	N	K	C	A	L	C	A
CCA	GTC	CGT	GGC	CCT	GAC	GGC	AGG	ATG	CAT	GGC	AAC	AAA	TGT	GCC	CTG	TGT	GCT
		784			793			802			811			820			829
F	K	R	R	F	S	E	E	N	S	K	T	D	Q	N	L	G	K
TTC	AAG	CGG	CGT	TTT	TCA	GAG	GAA	AAC	AGT	AAA	ACA	GAT	CAA	AAT	TTG	GGA	AAA
		844			853			862			871			880			889
Repeat 4																	
E	K	T	K	V	K	R	E	I	V	K	L	C	S	Q	Y	Q	N
GAA	AAA	ACT	AAA	GTT	AAA	AGA	GAA	ATT	GTG	AAA	CTC	TGC	AGT	CAA	TAT	CAA	AAT
		904			913			922			931			940			949

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K	N	G	I	L	F	C	T	R	E	N	D	P	I	R	G	P	D	G	K
AAG	AAT	GGA	ATA	CTT	TTC	TGT	ACC	AGA	GAA	AAT	GAC	CCT	ATT	CGT	GGT	CCA	GAT	GGG	AAA
		964			973			982			991			1000			1009		

M	H	G	N	L	C	S	M	C	Q	V	Y	F	Q	A	E	N	E	E	K
ATG	CAT	GGC	AAC	TTG	TGT	TCC	ATG	TGT	CAA	GTC	TAC	TTC	CAA	GCA	GAA	AAT	GAA	GAA	AAG
		1024			1033			1042			1051			1060			1069		

K	K	A	E	A	R	A	R	N	K	R	E	S	G	K	A	T	S	Y	A
AAA	AAG	GCT	GAA	GCA	CGA	GCT	AGA	AAC	AAA	AGA	GAA	TCT	GGA	AAA	GCA	ACC	TCA	TAT	GCA
		1084			1093			1102			1111			1120			1129		

Repeat 5

E	L	C	N	E	Y	R	K	L	V	R	N	G	K	L	A	C	T	R	E
GAG	CTT	TGC	AAT	GAA	TAT	CGA	AAG	CTT	GTG	AGG	AAC	GGA	AAA	CTT	GCT	TGC	ACC	AGA	GAG
		1144			1153			1162			1171			1180			1189		

N	D	P	I	Q	G	P	D	G	K	V	H	G	N	T	C	S	M	C	E
AAC	GAT	CCT	ATC	CAG	GGC	CCA	GAT	GGG	AAA	GTG	CAC	GGC	AAC	ACC	TGC	TCC	ATG	TGT	GAG
		1204			1213			1222			1231			1240			1249		

V	F	F	Q	A	E	E	E	E	K	K	K	K	E	G	E	S	R	N	K
GTC	TTC	TTC	CAA	GCA	GAA	GAA	GAA	GAA	AAG	AAA	AAG	AAG	GAA	GGC	GAA	TCA	AGA	AAC	AAA
		1264			1273			1282			1291			1300			1309		

Repeat 6

R	Q	S	K	S	T	A	S	F	E	E	L	C	S	E	Y	R	K	S	R
AGA	CAA	TCT	AAG	AGT	ACA	GCT	TCC	TTT	GAG	GAG	TTG	TGT	AGT	GAA	TAC	CGC	AAA	TCC	AGG
		1324			1333			1342			1351			1360			1369		

K	N	G	R	L	F	C	T	R	E	N	D	P	I	Q	G	P	D	G	K
AAA	AAC	GGA	CGG	CTT	TTT	TGC	ACC	AGA	GAG	AAT	GAC	CCC	ATC	CAG	GGC	CCA	GAT	GGG	AAA
		1384			1393			1402			1411			1420			1429		

M	H	G	N	T	C	S	M	C	E	A	F	F	Q	Q	E	E	R	A	R
ATG	CAT	GGC	AAC	ACC	TGC	TCC	ATG	TGT	GAG	GCC	TTC	TTT	CAA	CAA	GAA	GAA	AGA	GCA	AGA
		1444			1453			1462			1471			1480			1489		

Repeat 7

A	K	A	K	R	E	A	A	K	E	I	C	S	E	F	R	D	Q	V	R
GCA	AAG	GCT	AAA	AGA	GAA	GCT	GCA	AAG	GAA	ATC	TGC	AGT	GAA	TTT	CGG	GAC	CAA	GTG	AGG
		1504			1513			1522			1531			1540			1549		

N	G	T	L	I	C	T	R	E	H	N	P	V	R	G	P	D	G	K	M
AAT	GGA	ACA	CTT	ATA	TGC	ACC	AGG	GAG	CAT	AAT	CCT	GTC	CGT	GGA	CCA	GAT	GGC	AAA	ATG
		1564			1573			1582			1591			1600			1609		

H	G	N	K	C	A	M	C	A	S	V	F	K	L	E	E	E	E	K	K
CAT	GGA	AAC	AAG	TGT	GCC	ATG	TGT	GCC	AGT	GTG	TTC	AAA	CTT	GAA	GAA	GAA	GAG	AAG	AAA
		1624			1633			1642			1651			1660			1669		

N	D	K	E	E	K	G	K	V	E	A	E	K	V	K	R	E	A	V	Q
AAT	GAT	AAA	GAA	GAA	AAA	GGG	AAA	GTT	GAG	GCT	GAA	AAA	GTT	AAG	AGA	GAA	GCA	GTT	CAG
		1684			1693			1702			1711			1720			1729		

Repeat 8

E	L	C	S	E	Y	R	H	Y	V	R	N	G	R	L	P	C	T	R	E
GAG	CTG	TGC	AGT	GAA	TAT	CGT	CAT	TAT	GTG	AGG	AAT	GGA	CGA	CTC	CCC	TGT	ACC	AGA	GAG
		1744			1753			1762			1771			1780			1789		

N	D	P	I	E	G	L	D	G	K	I	H	G	N	T	C	S	M	C	E
AAT	GAT	CCT	ATT	GAG	GGT	CTA	GAT	GGG	AAA	ATC	CAC	GGC	AAC	ACC	TGC	TCC	ATG	TGT	GAA
		1804			1813			1822			1831			1840			1849		

A	F	F	Q	Q	E	A	K	E	K	E	R	A	E	P	R	A	K	V	K
GCC	TTC	TTC	CAG	CAA	GAA	GCA	AAA	GAA	AAA	GAA	AGA	GCT	GAA	CCC	AGA	GCA	AAA	GTC	AAA
		1864			1873			1882			1891			1900			1909		

Repeat 9

R	E	A	E	K	E	T	C	D	E	F	R	R	L	L	Q	N	G	K	L
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---

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AGA GAA GCT GAA AAG GAG ACA TGC GAT GAA TTT CGG AGA CTT TTG CAA AAT GGA AAA CTT
 1924 1933 1942 1951 1960 1969

#

F C T R E N D P V R G P D G K T H G N K
 TTC TGC ACA AGA GAA AAT GAT CCT GTG CGT GGC CCA GAT GGC AAG ACC CAT GGC AAC AAG
 1984 1993 2002 2011 2020 2029

#

C A M C K A V F Q K E N E E R K R K E E
 TGT GCC ATG TGT AAG GCA GTC TTC CAG AAA GAA AAT GAG GAA AGA AAG AGG AAA GAA GAG
 2044 2053 2062 2071 2080 2089

E D Q R N A A G H G S S G G G G G N T Q
 GAA GAT CAG AGA AAT GCT GCA GGA CAT GGT TCC AGT GGT GGT GGA GGA GGA AAC ACT CAG
 2104 2113 2122 2131 2140 2149

Repeat 10

#

D E C A E Y Q E Q M K N G R L S C T R E
 GAC GAA TGT GCT GAG TAT CAG GAA CAA ATG AAA AAT GGA AGA CTC AGC TGT ACT CGG GAG
 2164 2173 2182 2191 2200 2209

#

S D P V R D A D G K S Y N N Q C T M C K
 AGT GAT CCT GTA CGT GAT GAT GGC AAA TCG TAC AAC AAT CAG TGT ACC ATG TGT AAA
 2224 2233 2242 2251 2260 2269

A K L E R E A E R K N E Y S R S R S N G
 GCA AAA TTG GAA AGA GAA GCA GAG AGA AAA AAT GAG TAT TCT CGC TCC AGA TCA AAT GGG
 2284 2293 2302 2311 2320 2329

Repeat 11

#

T G S E S G K D T C D E F R S Q M K N G
 ACT GGA TCA GAA TCA GGG AAG GAT ACA TGT GAT GAG TTT AGA AGC CAA ATG AAA AAT GGA
 2344 2353 2362 2371 2380 2389

#

K L I C T R E S D P V R G P D G K T H G
 AAA CTT ATC TGC ACT CGA GAA AGT GAC CCT GTC CGG GGT CCA GAT GGC AAG ACA CAT GGT
 2404 2413 2422 2431 2440 2449

#

N K C T M C K E K L E R E A A E K K K K
 AAT AAG TGT ACT ATG TGT AAG GAA AAA CTG GAA AGG GAA GCA GCT GAA AAA AAA AAG AAA
 2464 2473 2482 2491 2500 2509

E D E D R S N T G E R S N T G E R S N D
 GAG GAT GAA GAC AGG AGC AAT ACA GGA GAA AGG AGC AAT ACA GGA GAA AGG AGC AAT GAC
 2524 2533 2542 2551 2560 2569

Repeat 12

#

K E D L C R E F R S M Q R N G K L I C T
 AAA GAG GAT CTG TGT CGT GAA TTT CGA AGC ATG CAG AGA AAT GGA AAG CTT ATC TGC ACC
 2584 2593 2602 2611 2620 2629

#

R E N N P V R G P Y G K M H I N K C A M
 AGA GAA AAT AAC CCT GTT CGA GGC CCA TAT GGC AAG ATG CAC ATC AAT AAA TGT GCT ATG
 2644 2653 2662 2671 2680 2689

#

C Q S I F D R E A N E R K K K D E E K S
 TGT CAG AGC ATC TTT GAT CGA GAA GCT AAT GAA AGA AAA AAG AAA GAT GAA GAG AAA TCA
 2704 2713 2722 2731 2740 2749

Repeat 13

#

S S K P S N N A K D E C S E F R N Y I R
 AGT AGC AAG CCC TCA AAT AAT GCA AAG GAT GAG TGC AGT GAA TTT CGA AAC TAT ATA AGG
 2764 2773 2782 2791 2800 2809

#

N N E L I C P R E N D P V H G A D G K F
 AAC AAT GAA CTC ATC TGC CCT AGA GAG AAT GAC CCA GTG CAC GGT GCT GAT GGA AAG TTC
 2824 2833 2842 2851 2860 2869

#

Y T N K C Y M C R A V F L T E A L E R A
 TAT ACA AAC AAG TGC TAC ATG TGC AGA GCT GTC TTT CTA ACA GAA GCT TTG GAA AGG GCA
 2884 2893 2902 2911 2920 2929

K L Q E K P S H V R A S Q E E D S P D S
 AAG CTT CAA GAA AAG CCA TCC CAT GTT AGA GCT TCT CAA GAG GAA GAC AGC CCA GAC TCT
 2944 2953 2962 2971 2980 2989

typical Kazal domain 2

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      *
F  S  S  L  D  S  E  M  C  K  D  Y  R  V  L  P  R  I  G  Y
TTC AGT TCT CTG GAT TCT GAG ATG TGC AAA GAC TAC CGA GTA TTG CCC AGG ATA GGC TAT
      3004      3013      3022      3031      3040      3049

#
L  C  P  K  D  L  K  P  V  C  G  D  D  G  Q  T  Y  N  N  P
CTT TGT CCA AAG GAT TTA AAG CCT GTC TGT GGT GAC GAT GGC CAA ACC TAC AAC AAT CCT
      3064      3073      3082      3091      3100      3109

#
C  M  L  C  H  E  N  L  I  R  Q  T  N  T  H  I  R  S  T  G
TGC ATG CTC TGT CAT GAA AAC CTG ATA CGC CAA ACA AAT ACA CAC ATC CGC AGT ACA GGG
      3124      3133      3142      3151      3160      3169

+
K  C  E  E  S  S  T  P  G  T  T  A  A  S  M  P  P  S  D  E
AAG TGT GAG GAG AGC AGC ACC CCA GGA ACC ACC GCA GCC AGC ATG CCC CCG TCT GAC GAA
      3184      3193      3202      3211      3220      3229

TGA CAG GAA GAT TGT TGA AAG CCA TGA GGG AAA AAA TAA ACC CCA GTT CTG AAT CAC CTA
      3244      3253      3262      3271      3280      3289

CCT TCA CCA TCT GTA TAT ACA AAG AAT TCT TCG GAG CTT GTC TTA TTT GCT ATA GAA AAC
      3304      3313      3322      3331      3340      3349

AAT ACA GAG CTT TTG GGA ATG GAA TCA CTG ATT TTC AGT CTT TTC CAT TTC TTT CCT CCT
      3364      3373      3382      3391      3400      3409

AGA ATC TGT GAT CTG AGG GTA TAA AGA CAT TTC CAC CAA GTT TGA GCC CTC AAA ATG TCC
      3424      3433      3442      3451      3460      3469

polyadenylation signal
TGA TTA CAA TGC TGT CTG TCC AAC TGC CTG TTC AAT AAA AGT AAA CTC AGC AGA AAA....
      3484      3493      3502      3511      3520      3529

```

.....poly(A) tail

The following sequence corrections have been performed:

An additional A in position 2510 results in a frame shift which produces three additional inhibitor domains.

Base were exchanged in ten different positions:

Position 551: G for A
 Position 1207: C for T
 Position 1258: C for T
 Position 1261: C for T
 Position 2175: A for G
 Position 2950: G for A
 Position 3228: C for T
 Position 3284: C for T
 Position 3324: C for T
 Position 3337: C for T

SEQUENZPROTOKOLL

<110> Forssmann Prof., Wolf-Georg

<120> Serin-Proteinase-Inhibitoren

<130> Forssmann

<140>

<141>

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<170> PatentIn Ver. 2.1

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